EXHIBIT 6

DeCypher Results for Job: Smith-Waterman Similarity Search

Results by Query

Click on a query below to view its search results.

1394_PTH9903

Search Details

Results for: 1394_PTH9903; (Length=669/QuerySize=669)

Return to query summary

```
Maximum possible score for this scoring matrix and query: 6690.00

RANK     SCORES QF TARGET LOCUS NAME                    ACCESSION# TF TARGET
P_SCORE DESCRIPTION
1       3455.00  C gi|1787371|gb|AE000213.1|AE00021 AE000213.1   D
ecoli_ae  -1.0e+00 Escherichia coli K12 MG1655 section 103 of 400 of th
2        246.00  D gi|1787371|gb|AE000213.1|AE00021 AE000213.1   D
ecoli_ae  -1.0e+00 Escherichia coli K12 MG1655 section 103 of 400 of th
```

```
RANK 1 Score =  3455.00  P_Score =  -1.0e+00
 Q = CGI_3078ws206512.seq              QF =  C #Q Symbols = 669
 T = gi|1787371|gb|AE000213.1|AE00021 TF =  D #T Symbols = 10959
 A = AE000213.1
 D = Escherichia coli K12 MG1655 section 103 of 400 of the complete
genome
 Identical Match = 500  Similar = 500  Total # Of Gaps = 4
 Identity: Alignment = 75% Query = 74% Target = 4%
 Similarity: Alignment = 75% Query = 74% Target = 4%
 QS =     662  QE =      1  TS =     8606  TE =     9268

Q     662 TCCTT-AGGGGTAACATCCCGCCATTCCCCGTTTGCCAGCGAGTCCAGCGTATAGCTGCC
          TCCTT A   GT AC TC CGCCATTC CC TT GC AG    TCCA  G  TA    CC
T    8606 TCCTTAATCTGTCACTTCTCGCCATTCACCATTGGCAAGATTATCCAAAGAGTAATCACC

Q     603 CATGGCGTAGCGAATGAGTCGCAGGGTAGGGAAGCCCACATGCGCAGTCATGCGCCTGAC
```

```
             CAT GC TAGCGAAT AGTCGCAG GT GGGAAGCC ACATG GC GTCATGCG C  AC
T     8666   CATCGCATAGCGAATCAGTCGCAGCGTGGGGAAGCCAACATGGGCGGTCATGCGGCGCAC

Q     543    CTGTCGGTTGCGGCCTTCATAAAGGGTGATTTTAAGCCAGCTGGTAGGAATGGATTTACG
             CTG CG TT CG CCTTCATA A GGTGAT TT AGCCAGCTGGT GGAAT   TTT CG
T     8726   CTGGCGATTACGTCCTTCATATAAGGTGATCTTCAGCCAGCTGGTGGGAATACTTTTGCG

Q     483    CTCACGAATCGGCGGGTTGCGCGGCCACAGCCACTCGGGTTCATTCACACGTTCAATACC
             TCACGAAT GG GG TT CGCGGCCA A CCAC CGGGTTC T AC G TC    CC
T     8786   TTCACGAATTGGTGGATTCCGCGGCCATAACCACGCGGGTTCGTCAACCAGCTCCGCGCC

Q     423    AGCCGGCAGGGTGGGACCGTCGTTCAGCGTTACGCCGTTGCGCA--GCTTTGCCAGCGAC
             GC GGCAGGGT GG CC TC TT A GTTACGCC TTGCGCA  GCTT    GCG C
T     8846   GGCGGGCAGGGTAGGGCCATCATTTAAGGTTACGCCATTGCGCAAGGCTTCAAGTGCGTC

Q     365    GCGTCGTCCGGCTCGCCTTCAACCTGCACATAGTAAATTTTTCCGGTACGTTTGCCCGGC
              GT GT  GG   CCTTC ACCTGCACATA TA ATTTTTCCGGT CGTTT CCCGGC
T     8906   TTGT-GT-GGGAATACCTTCCACCTGCACATAATAGATTTTTCCGGTGCGTTTACCCGGC

Q     305    TGAGTAAGCCTGGCCTGGAGCACGCCGTCATTGGTAAGGACCAGCAGCCCCTCGCTGTCG
             TG GT A  C  GCCTG A C CGCCGT ATTGGT AG ACCAGCA CCC TCGCT TCG
T     8964   TGGGTTAAACGCGCCTGCAACGCGCCGTTATTGGTCAGCACCAGCAACCCTTCGCTATCG

Q     245    CGATCCAGACGTCCCGCTGCGTAGACTCCCTGTACGGGGATAAAGTCCTTCAGCGTGCTG
             CG TC AG CG CC GCTGC TA AC CCCTG AC GGGAT AA TC TT A GT  TG
T     9024   CGGTCAAGGCGACCTGCTGCATAAACACCCTGAACCGGGATGAATTCTTTTAATGTTTTG

Q     185    CGCCCGGCCTCGTCGGTAAACTGCGGCAATACATCGTAGGGTTTATTGAACAGTATGACC
             CG CCGGC TC TCGGT AACTGCGG A  ACATCGTAGGGTTTATTGAACAG AT AC
T     9084   CGTCCGGCTTCATCGGTGAACTGCGGAAGAACATCGTAGGGTTTATTGAACAGGATCACA

Q     125    CGCGTTGGCTGGGGGTTCTGGCGTTCTTCTGGTGGCTTGTCGTGAGCTGAATCGCTCAACC
             CGCGT GGCTGG  TTC GG  T C CTGGT G  GT G GAGCTGAATCGCT AACC
T     9144   CGCGTGGGCTGGTTTTCAGGTTTACGCCTGGTAGAACGTTGCGAGCTGAATCGCTTAACC

Q     65     CGGTGTTTTCTAAAAGAAGTTTTCGTCATGGTATTTTCAGGCGTTATCAATTGCCGCATT
             GGTG TTTCTAAAAGAAGTTTT  CATGGTATTTTCAG  TTAT AATTGCCGCATT
T     9204   TGGTGATTTCTAAAAGAAGTTTTTTGCATGGTATTTTCAGAGATTATGAATTGCCGCATT

Q     5      ATAGC
             ATAGC
T     9264   ATAGC
```

```
Q     234 ACGTCTGGATCGCGACAGCGAGGGGCTGCTGGTCCTTACCAATGACGGCGTGCTCCAGGC
          ACGTCTGG TCG G CAGCGA  G  T  C  G    TT C AA GA    CGTG   C G
T   10054 ACGTCTGGTTCGTG-CAGCGATCGAATAC--GCAATTGCTAACGA--TCGTGACTCTG--

Q     294 CAGGCTTACTCAGCCGGGCAAACGTACCGGAA--AAATTTAC--TATGTGCAGGTTGAAG
           T ACTC  G  G  CAAA G A C   A  AA TT AC   A G GC G TT AAG
T   10107 -----TGACTCTGGTGCACAAAGGCAACATCATGAAGTTCACCGAAGGAGC-GTTTAAAG

Q     350 GCGAGCCGGACGACGCGTCGCTGGCAAAGCTGCGCAACGGCGTAACGCTGAACGACGGTC
            C G   AC A   G CGC  G A AG T  G   CGG G A   CTGA CGACGGT
T   10161 ACTGGGGCTACCAGCTGGCGCGTGAAGAGTTTGG---CGGTGAA---CTGATCGACGGTG

Q     410 CCACCCTGCCGGCTGGTATTGAACGTGTGAATGAACCCGAGTGGCTGTGGCCGCGCAACC
           C CC TG C            TGAA GT T AA  AACCCGA   C TGGC   G  A C
T   10215 GC-CCGTGGC---------TGAAAGT-TAAA--AACCCGA---ACACTGGCAAAGAGATC

Q     470 CGCCGATT-----CGTGAGCGTAAATCCATTCCT--ACCAG-----------CTGGCTT
           C ATT     CGTGA G  AT CATTCCT  A CAG         C GGCT
T   10259 GTC--ATTAAAGACGTGATTGCTGATGCATTCCTGCAACAGATCCTGCTGCGTCCGGCTG

Q     511 AAAATCA-------CCCTTTATGAAGGCCGCAAC-----CGACAGGTCAGGCG-CATGAC
          AA AT A       CCT TATGAA CC AAC    C ACA  TC G CG C TG C
T   10317 AATATGATGTTATCGCCTGTATGAA--CCTGAACGGTGACTACATTTCTGACGCCCTGGC

Q     558 TGCGCATGTGGGC
          GCGCA GT GGC
T   10375 AGCGCAGGTTGGC
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Job Details

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[BEGIN JOB STATUS]

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[END SEARCH TIME] Fri Dec 06 12:44:24 2002
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[EOL] CRLF
[CGI INTERFACE VERSION] 2
[CGI JOB TITLE] Smith-Waterman Similarity Search
[COMMENT] /CGI_Ver=7.2.3.242
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[EXTEND PENALTY] -5
[FRAME PENALTY] 0
[QUERY FORMAT] FASTA/PEARSON
[QUERY TYPE] NT

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[QUERY SET] CGI_3078ws206512.seq
[TARGET TYPE] NT
[TARGET FRAMES] D
[TARGET PATH] d:\decypher\target
[OUTPUT FORMAT] COUNTDOWNCOMPLEMENT [USE SYSTEM] tblast-m
[TARGET SET] d:\decypher\target\ecoli_ae000213.txt
[SIGNIFICANCE] GAPPED
[MAX SCORES] 30
[MAX ALIGNMENTS] 20
[THRESHOLD] 1
[ALIGNMENT THRESHOLD] 20
[RESULT PATH] d:\decypher\output
[HTML RESULT PATH] C:\WebSite\cgi-temp\3078ws.out
[OUTPUT FORMAT] TEXT MAXSCORE PERCENTAGE EXTRACTALIGNED MATCHCHARACTER
[OUTPUT FORMAT] HTML WEB
[CGI REFERING PAGE] http://tblast-m.genomecorp.com/algo-sw/sw_nn.shtml
[CGI COOKIE] Set-Cookie: DeCypher=; expires=Saturday, 06-Dec-03
12:00:00 GMT; path=/; domain=tblast-m.genomecorp.com;


[JOB MESSAGES]


[END JOB STATUS]
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For assistance contact
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